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10/618,320 G proteins, polynucleotide encoding the same and utilization thereof

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1	333673	60,638	<a href="#">C</a>
1	333674	60,638	<a href="#">C</a>
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1	333677	60,638	<a href="#">C</a>
1	333678	60,638	<a href="#">C</a>
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10/618,320

## G proteins, polynucleotide encoding the same and utilization the

GenCore version 5.1.7

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2006, 19:29:36 ; Search time 142.364 Seconds  
 (without alignments)  
 1413.528 Million cell updates/sec

Title: US-10-618-320A-1

Perfect score: 2400

Sequence: 1 MGLCYSLRPLLFGGPQDPC.....VFNDICRDIQIQRMHLKQYELL 458

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_21:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2400	100.0	458	8	ADG74722	Adg74722 Human G-p
2	2400	100.0	458	9	AEA17292	Aea17292 Human XIG
3	2124	88.5	448	8	ADG74746	Adg74746 Mouse G-p
4	2113	88.0	450	8	ADG74747	Adg74747 Rat G-pro
5	1819	75.8	381	5	ABB09272	Abb09272 G protein
6	1819	75.8	381	7	ADC09607	Adc09607 Human G-p
7	1819	75.8	381	7	ADE61907	Ade61907 Human Pro
8	1819	75.8	381	8	ADU60726	Adu60726 Human G-p
9	1819	75.8	381	9	ADX26261	Adx26261 Novel cel
10	1819	75.8	381	9	AEA17294	Aea17294 Human Gol
11						

## SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	

1	2400	100.0	458	8	ADG74722	Adg74722 Human G-P
2	2400	100.0	458	9	AEA17292	Aea17292 Human XLG
3	2124	88.5	448	8	ADG74746	Adg74746 Mouse G-p
4	2113	88.0	450	8	ADG74747	Adg74747 Rat G-pro
5	1819	75.8	381	5	ABB09272	Abb092 1811 75.5 381 7 A
12	1559	65.0	756	5	ABG60299	Abg60299 Lymphoma
13	1559	65.0	756	6	ABP97657	Abp97657 Amino aci
14	1559	65.0	909	8	ADQ26060	Adg26060 Guanine n
15	1559	65.0	909	8	ABM82265	Abm82265 Tumour-as
16	1559	65.0	909	9	ADX06936	Adx06936 Cyclin-de
17	1540	64.2	379	4	AAB99060	Aab99060 Human G-p
18	1540	64.2	379	5	ABB09269	Abb09269 G protein
19	1540	64.2	379	7	ADC09604	Adc09604 Human G-p
20	1540	64.2	379	7	ADJ68299	Adj68299 Human hea
21	1540	64.2	379	8	ADU60723	Adu60723 Human G-p
22	1537	64.0	720	6	ABP56694	Abp56694 GCR1:Gs f
23	1536.5	64.0	755	8	ADM79379	Adm79379 Mouse lym
24	1529.5	63.7	380	3	AAB23382	Aab23382 Human G-a
25	1529.5	63.7	380	4	AAB99058	Aab99058 Human G-p
26	1529.5	63.7	380	4	AAB99061	Aab99061 Human G-p
27	1529.5	63.7	380	5	ABB09270	Abb09270 G protein
28	1529.5	63.7	380	7	ADC09605	Adc09605 Human G-p
29	1529.5	63.7	380	7	ADP70778	Adp 70778 Cyclin-de
17	1540	64.2	379	4	AAB99060	Aab99060 Human G-p
18	1540	64.2	379	5	ABB09269	Abb09269 G protein
19	1540	64.2	379	7	ADC09604	Adc09604 Human G-p
20	1540	64.2	379	7	ADJ68299	Adj68299 Human hea
21	1540	64.2	379	8	ADU60723	Adu60723 Human G-p
22	1537	64.0	720	6	ABP56694	Abp56694 GCR1:Gs f
23	1536.5	64.0	755	8	ADM79379	Adm79379 Mouse lym
24	1529.5	70778 Minicell				
30	1529.5	63.7	380	8	ADQ26061	Adq26061 Guanine n
31	1529.5	63.7	380	8	ABM82267	Abm82267 Tumour-as
32	1529.5	63.7	380	8	ADU60724	Adu60724 Human G-p
33	1526.5	63.6	926	4	AAU04387	Aau04387 GPCR-Gs f
34	1526.5	63.6	926	7	ADL96550	Adl96550 G protein
35	1526.5	63.6	926	9	ADW44723	Adw44723 Human RUP
36	1526.5	63.6	926	9	AEB20907	Aeb20907 Human RUP
37	1525.5	63.6	394	2	AAR94559	Aar94559 Human Gs
38	1525.5	63.6	394	5	ABB09267	Abb09267 G protein
39	1525.5	63.6	394	5	ABG60304	Abg60304 Lymphoma
40	1525.5	63.6	394	6	ABP97662	Abp97662 Amino aci
41	1525.5	63.6	394	7	ABR82636	Abr82636 C. elegan
42	1525.5	63.6	394	7	ADC09602	Adc09602 Human G-p
43	1525.5	63.6	394	7	ADP70779	Adp70779 Minicell
44	1525.5	63.6	394	8	ADQ26059	Adq26059 Guanine n
45	1525.5	63.6	394	8	ABM82266	Abm82266 Tumour-as

## ALIGNMENTS

RESULT 1  
 ADG74722  
 ID ADG74722 standard; protein; 458 AA.  
 XX  
 AC ADG74722;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Human G-protein Gml amino acid sequence.  
 XX  
 KW G protein; Gml; G protein-coupled receptor mediated signal transduction;  
 KW GTP binding site; GTPase site; G protein alpha subunit;  
 KW signal transduction; G-protein-coupled receptor.  
 XX

SQ Sequence 458 AA;

Query Match 100.0%; Score 2400; DB 9; Length 458otein coupled receptors (GPC  
 CC that the N-terminus of the XLGolf protein is altered compared to Golf  
 CC with a different exon 1. Specifically, it refers to contacting the GPCR  
 CC with a test compound, and determining GPCR activity, where a change in  
 CC activity indicates that the compound is a modulator thereof. The present  
 CC invention describes the GPCR as a Gs coupled GPCR that is selected from  
 CC dopamine receptor D1, adenosine A2a receptor, and adrenergic beta-2  
 CC receptor. Accordingly, the composition and methods are useful for  
 CC identifying modulators of GPCR activity, as well as for diagnosing or  
 CC treating schizophrenia and other psychiatric disorders. Furthermore, the  
 CC pharmaceutical compositions derived thereof exhibit neuroleptic activity  
 CC and can be used for gene therapy purposes. This polypeptide sequence is  
 CC th;

Best Local Similarity 100.0%; Pred. No. 6.3e-200;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLCYSLRPLLFFGGPGDDPCAASEPPVEDAQPAPAPALAPVRAAARDTARTLLPRGEGGS 60  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 1 MGLCYSLRPLLFFGGPGDDPCAASEPPVEDAQPAPAPALAPVRAAARDTARTLLPRGEGGS 60  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 61 PACARPkadkpkekrqrteqlsaeereakereavkearkvsvrgidrmlrdqkrdlqqth 120  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 61 PACARPkadkpkekrqrteqlsaeereakereavkearkvsvrgidrmlrdqkrdlqqth 120  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 121 RLLLLGAGESGKSTIVKQMRILHVNGFNPEEKQKILDIRKVNVDKDAIVTIVSAMSTIIPP 180  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 121 RLLLLGAGESGKSTIVKQMRILHVNGFNPEEKQKILDIRKVNVDKDAIVTIVSAMSTIIPP 180  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 181 VPLANPENQFRSDYIKSIAPITDPEYSQEFPDVHKVLWDDEGVKACFERSNEYQLIDCAQ 240  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 181 VPLANPENQFRSDYIKSIAPITDPEYSQEFPDVHKVLWDDEGVKACFERSNEYQLIDCAQ 240  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 241 YFLERIDSVSLSVDTPTDQDLLRCRVLTSGIFETRQFQVDKVNHFMDVGGQRDERRKWIQ 300  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 241 YFLERIDSVSLSVDTPTDQDLLRCRVLTSGIFETRQFQVDKVNHFMDVGGQRDERRKWIQ 300  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 301 CFNDVTAIYVAACSSYNMVIREDNNNTNRLRESLDLFEISINNNRWLRTISIILFLNKQDM 360  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/KRDQLQQTH 120  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 61 PACARPkadkpkekrqrteqlsaeereakereavkearkvsvrgidrmlrdqkrdlqqth 120  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 121 RLLLLGAGESGKSTIVKQMRILHVNGFNPEEKQKILDIRKVNVDKDAIVTIVSAMSTIIPP 180  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 121 RLLLLGAGESGKSTIVKQMRILHVNGFNPEEKQKILDIRKVNVDKDAIVTIVSAMSTIIPP 180  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 181 VPLANPENQFRSDYIKSIAPITDPEYSQEFPDVHKVLWDDEGVKACFERSNEYQLIDCAQ 240  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 181 VPLANPENQFRSDYIKSIdb 301 CFNDVTAIYVAACSSYNMVIREDNNNTNRLRESLDLFEISINNNRWLRTISIILFLNKQDM 360  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 361 LAEKVLAGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 361 LAEKVLAGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Qy 421 HYCYPHPTCAVDTENIRRVFNDRCRDIQIQRMLHLQYELL 458  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/Db 421 HYCYPHPTCAVDTENIRRVFNDRCRDIQIQRMLHLQYELL 458  
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/

RESULT 3

ADG74746

ID ADG74746 standard; protein; 448 AA.

XX

AC ADG74746;



Db	171	VPLANPENQFRSDYIKSIAPITDPEYSEQEFDHVKKLWDDEGVKACFRSNEYQLIDCAQ	230
Qy	241	YFLERIDSVSLVDTPTDQDLLRCRVLTSGLFETRFPQVDKVNFMFDVGGQRDERRKWIQ	300
Db	231	YFLERIDSVSLVDTPTDQDLLRCRVLTSGLFETRFPQVDKVNFMFDVGGQRDERRKWIQ	290
Qy	301	CFDNDVTAIIYVAASSYNNMIREDDNNTNRLRESLDLFESIWNRRWLRTISIILPLNKQDM	360
Db	291	CFNDVTAIIYVAASSYNNMIREDDNNTNRLRESLDLFESIWNRRWLRTISIILPLNKQDM	350
Qy	361	LAEKVLAGKSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFRLRISTATGDGK	420
Db	351	LAEKVLAGKSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFRLRISTATGDGK	410
Qy	421	HYCYPHFTCAVDTENIRRVPNDRCDIIQRMHLKQYELL	488
Db	411	HYCYPHFTCAVDTENIRRVPNDRCDIIQRMHLKQYELL	448

RESULT 4  
 ADG74747  
 ID ADG74747 standard; protein; 450 AA.  
 XX  
 AC ADG74747;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Rat G-protein Gm1 amino acid sequence.  
 XX  
 KW G protein; Gm1; G protein-coupled receptor mediated signal transduction;  
 KW GTP binding site; GTPase site; G protein alpha subunit;  
 KW signal transduction; G-protein-coupled receptor; rat.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN EP1382613-A1.  
 XX  
 PD 21-JAN-2004.  
 XX  
 PF 09-JUL-2003; 2003EP-00015519.  
 XX  
 PR 16-JUL-2002; 2002JP-00206841.  
 PR 19-DEC-2002; 2002JP-00367778.  
 PR 31-MAR-2003; 2003JP-00095955.  
 XX  
 PA (SUMO ) SUMITOMO CHEM CO LTD.  
 XX  
 PI Takahashi Y, Matsumoto Y, Oeda K;  
 XX  
 DR WPI; 2004-111483/12.  
 DR N-PSDB; ADG74749.  
 XX  
 PT New protein useful as a therapeutic or prophylactic agent against a  
 PT disease caused by an abnormality in a G-protein coupled receptor mediated  
 PT signal transduction.  
 XX  
 PS Claim 1; SEQ ID NO 26; 85pp; English.  
 XX  
 CC This invention relates to a novel G protein (Gm1). The protein is  
 CC involved in a G protein-coupled receptor mediated signal transduction.  
 CC The protein of the invention has a sequence with a high homology with a  
 CC GTP binding site and a GTPase site conserved among G protein alpha  
 CC subunits. The protein, the DNA sequence which encodes it and an antibody  
 CC specifically recognising the protein of the invention may be useful as a  
 CC therapeutic or prophylactic agent against a disease caused by an

CC abnormality in a G-protein coupled receptor mediated signal transduction.  
 CC The invention may also be useful for screening for a substance capable of  
 CC regulating a signal transduction mediated by a G-protein-coupled receptor  
 CC and a protein. The present sequence is that of the rat Gm1 protein which  
 CC is related to the human Gm1 protein of the invention.  
 XX

SQ Sequence 450 AA;

Query Match 88.0%; Score 2113; DB 8; Length 450;  
 Best Local Similarity 90.2%; Pred. No. 6.1e-175;  
 Matches 415; Conservative 7; Mismatches 26; Indels 12; Gaps 4;

Qy 1 MGLCYSLRPLLFGGGPDDPCAASEPPVEDAQP--APAPALAPVRAAARDTARTLLPRGGE 58  
 ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

Db 1 MGLCYSLRPLLFGGSDAPCEPCEPCEAEDAQPSSAAPAPAPAPIPAPA --PVGTLRLRGDG 58

Qy 59 GSPACARPkadKPKERQRTEQLSAEERAAKEREAVKEARKVSRGIDRMLRDQKRDLQQ 118  
 ||| : - : - : - : - : - : - : - : - : - : - : - : - : - : - : - : - : - : -

Db 59 RIPASARSPV-E-LQNRRRQEQLRAEERAA-----KEARKVSRGIDRMLREQKRDLQQ 110

Qy 119 THRLLLLGGAGSGSGSTIVKQMRILHVNGFNPEEKKKQKILDIRKNVKDAVITIISAMSTII 178  
 ||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

Db 111 THRLLLLGGAGSGSGSTIVKQMRILHVNGFNPEEKKKQKILDIRKNVKDAVITIISAMSTII 170

Qy 179 PPVPLANPENQFRSDYIKSIAPITDPEYSQEFFDHDVKLWDRGVVKACFERSNEYQLIDC 238

Db 171 PPVPLANPENQFRSDYIKSIAPITDPEYSQEFFDHDVKLWDRGVVKACFERSNEYQLIDC 230

Qy 239 AQYFLERIDSVSVDYPTDQDLLECRVLTSGIFETRFQVDKVNPHMPDVGGQRDERRKW 298

Db 231 AQYFLERIDSVSVDYPTDQDLLECRVLTSGIFETRFQVDKVNPHMPDVGGQRDERRKW 290

Qy 299 IQCFCNDVTAIIYVAACSSYNNMVIREDNNNTNLRESLDFESIWNRRWLRTISIILFLNKQ 358

Db 291 IQCFCNDVTAIIYVAACSSYNNMVIREDNNNTNLRESLDFESIWNRRWLRTISIILFLNKQ 350

Qy 359 DMLAEKVLAGKS KIEDYFPEYANYTVPEADTPDAGEDPKVTRAKFFIRDLFLRISTATGD 418

Db 351 DMLAEKVLAGKS KIEDYFPEYANYTVPEADTPDAGEDPKVTRAKFFIRDLFLRISTATGD 410

Qy 419 GKHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458

Db 411 GKHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 450

RESULT 5

ABB09272

ID ABB09272 standard; protein; 381 AA.

XX

AC ABB09272;

XX

DT 10-JUL-2002 (first entry)

XX

DE G protein-coupled receptor (GPCR) >g-olff SEQ ID NO:18.

XX

KW Target activated nucleic acid biosensor; signalling moiety; GPCR;  
 KW nucleic acid sensor; detection; engineering; drug optimisation;  
 KW G protein-coupled receptor.

XX

OS Homo sapiens.

XX

PN WO200222882-A2.

XX

PD 21-MAR-2002.

XX

PF 13-SEP-2001; 2001WO-US028835.